

10/767.701

10/767.701

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 05:07:14 ; Search time 229 Seconds

(without alignments)
677.800 Million cell updates/sec

Title: US-10-767-701-44293
Perfect score: 1131
Sequence: 1 MGOQSLIVAFVARGVTILAE.....IIIALILITLSCVCHGPKCH 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 300 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1100	97.3	220	2	Q69MS1_ORYSA
2	1091	96.5	220	2	Q84S21_ORYSA
3	1016	89.8	285	1	VA725_ARATH
4	1010	89.3	219	1	VA721_ARATH
5	1010	89.3	219	2	Q681L9_ARATH
6	1006	88.9	219	2	Q681H0_ARATH
7	1003	88.7	220	1	VA726_ARATH
8	995	88.0	221	1	VA722_ARATH
9	933	82.5	194	2	Q7X9C5_PIRYP
10	848.5	75.0	222	1	VA724_ARATH
11	848.5	75.0	222	2	Q6ID96_ARATH
12	795	70.3	215	2	Q5URW2_HORVD
13	792	70.0	217	1	VA723_ARATH
14	786	69.5	218	2	Q6RUK6_TRIMO
15	779	68.9	181	2	Q67YV9_ARATH
16	741.5	65.6	248	1	Q8H3D2_ORYSA
17	732.5	64.8	240	1	VA727_ARATH
18	732.5	64.8	240	2	Q53XB0_ARATH
19	715	63.2	241	2	Q6YZI8_ORYSA
20	413.5	36.6	219	1	VA713_ARATH
21	407	36.0	221	1	VA711_ARATH
22	396	35.0	221	1	VA714_ARATH
23	394.5	34.9	260	2	Q8EAC7_DICDI
24	387	34.2	220	2	Q6DDH7_XENTIA
25	384	34.0	220	2	Q5EL74_CHICK
26	383	33.9	220	2	P70280_MOUSE
27	380	33.6	219	1	SYBL1_HUMAN
28	380	33.6	220	2	Q53GY7_HUMAN
29	379	33.5	87	2	Q4U3F2_IPOBA
30	377.5	33.4	219	1	VA712_ARATH
31	377	33.3	219	1	SYBL1_PONPY

32	377	33.3	220	2	Q9JHM5_RAT
33	372	32.9	221	2	Q9LAK1_ORYSA
34	360	31.8	223	2	Q8670_ORYSA
35	346.5	30.6	226	2	Q69SJ1_ORYSA
36	343.5	30.4	218	2	Q9VSC3_DROME
37	338.5	29.9	228	2	Q7Z0P6_PARTH
38	338.5	29.9	306	2	Q560P1_CRYNE
39	338.5	29.9	306	2	Q5XDN6_CRYNE
40	338	29.9	208	2	Q8IET3_PLAF7
41	332	29.4	208	2	Q4YCD2_PLABE
42	327	28.9	216	2	Q5ANW7_DICDI
43	321	28.4	218	2	Q70BD7_ANOGA
44	302.5	26.7	242	2	Q7S9T6_NEUCR
45	299	26.4	236	2	Q41187_GIIZE
46	298	26.3	173	2	Q4T515_TETNG
47	290.5	25.7	209	2	Q4PHX9_USTMA
48	277.5	24.5	179	2	Q7Z409_HUMAN
49	271.5	24.0	253	2	Q4WM41_ASPEU
50	259.5	22.9	263	2	Q5BFRV_EMENT
51	258	22.8	210	2	Q7Z0P5_PARTH
52	255	22.5	210	2	Q7Z113_PARTH
53	255	22.5	230	2	Q52FF5_MAGGR
54	254	22.5	226	2	Q6CFT6_YARLI
55	252	22.3	255	2	Q7YY68_CRYPV
56	247	21.8	164	2	Q4X063_PLACH
57	245	21.7	206	2	Q9LXK2_ARATH
58	244	21.6	181	2	Q7ZU11_BRARE
59	242	21.6	223	2	Q8NKK9_ASPEU
60	237	21.0	260	2	Q9H4A7_HUMAN
61	237	21.0	260	2	Q5MDW3_TOBAN
62	217.5	19.3	75	2	Q7YUS4_GRYYP
63	215	19.0	221	2	Q5TUB0_GRYYP
64	214	18.9	216	2	Q4FY81_LBIMA
65	201.5	17.8	115	2	Q6CHZ4_YARLI
66	200.5	17.7	121	1	SYBL1_SCHPO
67	199	17.6	215	2	Q4QIG6_LBIMA
68	198.5	17.6	135	2	Q6BSW9_DBRHA
69	197.5	17.5	112	2	Q6C714_YARLI
70	195.5	17.3	257	2	Q4QC67_LBIMA
71	194.5	17.2	118	2	Q412M1_GIIBE
72	192.5	17.0	228	2	Q513U3_ENTHI
73	186	16.4	140	2	Q610B0_BRARE
74	185	16.4	117	1	SNCL1_YEAST
75	185	16.4	192	2	Q6EFX0_ENTHI
76	185	16.4	223	2	Q265B6_SCHMA
77	184.5	16.3	109	2	Q759C2_ASHGO
78	182	16.1	245	2	Q95XHI_CABEL
79	181.5	16.0	84	2	Q4S246_TETNG
80	181.5	16.0	124	2	Q7SF83_NEUCR
81	180	15.9	113	2	Q6FT06_CANCA
82	180	15.9	245	2	Q61HR8_CABER
83	178.5	15.8	111	2	Q6B781_TRIRE
84	178.5	15.8	120	2	Q5SLN4_CRYNE
85	178.5	15.8	120	2	Q5KD71_CRYNE
86	177.5	15.7	129	2	Q6X173_DROYA
87	177.5	15.7	129	2	Q9V516_DROME
88	177.5	15.7	132	2	Q6MKX1_DROME
89	177	15.6	119	2	Q7P1S4_ANOGA
90	176	15.6	119	2	Q7RH0_PLYAO
91	176	15.6	127	2	Q7PNS9_ANOGA
92	176	15.6	277	2	Q6ZC93_ORYSA
93	175	15.5	108	2	Q60WU2_CABER
94	175	15.5	109	2	Q02495_CABEL
95	174.5	15.4	115	1	SNCL2_YEAST
96	174.5	15.4	201	2	Q9CTX9_CABEL
97	174.5	15.4	231	2	Q6CTD6_KIULA
98	174	15.4	95	2	Q6TMA9_DICDI
99	173	15.3	180	1	SYB_APLCA
100	172.5	15.3	230	2	Q7Z0T4_ENTHI
101	172.5	15.3	230	2	Q51CN2_ENTHI
102	172	15.2	110	2	Q6CY19_KIULA
103	172	15.2	111	2	Q7PT71_ANOGA
104	172	15.2	145	2	Q869G4_LYMST

Q9JHM5	rattus norv
Q9LAK1	oryza sativ
Q8670	oryza sativ
Q69S1	oryza sativ
Q9VSC3	drosophila
Q7Z0P6	parametium
Q560P1	cryptococcu
Q5XDN6	cryptococcu
Q8IET3	plasmodium
Q4YCD2	plasmodium
Q5ANW7	dicystoceti
Q70BD7	anopheles g
Q7S9T6	neutrospora
Q41187	gliberella
Q4T515	tetragodon n
Q4PHX9	usiliago ma
Q7Z409	homo sapien
Q4WM41	aspergillus
Q5BFRV	aspergillus
Q7Z0P5	parametium
Q7Z113	parametium
Q52FF5	magnaporthe
Q6CFT6	yarrowia li
Q7YY68	cryptospori
Q4X063	plasmodium
Q9LXK2	arabidopsis
Q7ZU11	brachydanto
Q8NKK9	aspergillus
Q9H4A7	homo sapien
Q5MDW3	nicotiana t
Q7YUS4	trypanosoma
Q5TUB0	trypanosoma
Q4FY81	leishmania
Q6CHZ4	yarrowia li
Q412M1	gliberella
Q513U3	leishmania
Q610B0	brachydanto
P31109	saccharomye
Q86FX0	entamoeba h
Q265B6	saccharomye
Q759C2	asbya gose
Q95XHI	caenorhabdi
Q4S246	tetradodon n
Q7SF83	neutrospora
Q6FT06	candida gla
Q61HR8	caenorhabdi
Q6B781	trichoderma
Q5SLN4	cryptococcu
Q5KD71	cryptococcu
Q6X173	drosophila
Q9V516	drosophila
Q6MKX1	drosophila
Q7P1S4	anopheles g
Q7RH0	plasmodium
Q7PNS9	anopheles g
Q6ZC93	oryza sativ
Q60WU2	caenorhabdi
Q02495	caenorhabdi
P33328	saccharomye
Q9CTX9	caenorhabdi
Q6CTD6	kluyveromye
Q6TMA9	dictyoceti
Q6CY19	aplysia cal
Q7Z0T4	entamoeba h
Q51CN2	entamoeba h
Q6CY19	kluyveromye
Q7PT71	anopheles g
Q869G4	lymanaea sca

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OM: protein search, using sw model

Run on: March 2, 2006, 05:07:39 / Search time 186 Seconds

(without alignments)
519.695 Million cell updates/sec

Title: US-10-767-701-44293

Perfect score: 1131

Sequence: 1 MGQOSLIYAFVARGVTLAE.....IIIALIIILISVCHGFKCH 220

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database: A_Geneseq_21.*
1: geneseqp19808.*
2: geneseqp19908.*
3: geneseqp20008.*
4: geneseqp20018.*
5: geneseqp20028.*
6: geneseqp20038.*
7: geneseqp20048.*
8: geneseqp20058.*
9: geneseqp20068.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1131	100.0	244	8	ADY04217 Plant full
2	1131	100.0	244	8	ADY04217 Plant full
3	1131	100.0	244	8	ADY04217 Plant full
4	1131	100.0	244	8	ADY04217 Plant full
5	1131	100.0	244	8	ADY04217 Plant full
6	1131	100.0	244	8	ADY04217 Plant full
7	1131	100.0	244	8	ADY04217 Plant full
8	1131	100.0	244	8	ADY04217 Plant full
9	1131	100.0	244	8	ADY04217 Plant full
10	1131	100.0	244	8	ADY04217 Plant full
11	1131	100.0	244	8	ADY04217 Plant full
12	1131	100.0	244	8	ADY04217 Plant full
13	1131	100.0	244	8	ADY04217 Plant full
14	1131	100.0	244	8	ADY04217 Plant full
15	1131	100.0	244	8	ADY04217 Plant full
16	1131	100.0	244	8	ADY04217 Plant full
17	1131	100.0	244	8	ADY04217 Plant full
18	1131	100.0	244	8	ADY04217 Plant full
19	1131	100.0	244	8	ADY04217 Plant full
20	1131	100.0	244	8	ADY04217 Plant full
21	1131	100.0	244	8	ADY04217 Plant full
22	1131	100.0	244	8	ADY04217 Plant full
23	1131	100.0	244	8	ADY04217 Plant full
24	1131	100.0	244	8	ADY04217 Plant full

25	784	69.3	232	8	ADY67636	ADY67636 Plant full
26	744	65.8	155	3	AAB32593	AAB32593 Eucalyptu
27	740	65.4	161	3	AAB32883	AAB32883 Pinus rad
28	732.5	64.8	240	3	AAG54006	AAG54006 Arabidops
29	732.5	64.8	240	3	AAG54005	AAG54005 Arabidops
30	732.5	64.8	240	3	AAG54008	AAG54008 Arabidops
31	732.5	64.8	240	3	AAG54005	AAG54005 Arabidops
32	732.5	64.8	240	3	AAG54008	AAG54008 Arabidops
33	732.5	64.8	240	3	AAG54005	AAG54005 Arabidops
34	732.5	64.8	240	3	AAG54008	AAG54008 Arabidops
35	732.5	64.8	240	3	AAG54005	AAG54005 Arabidops
36	718	63.5	166	3	AAG30423	AAG30423 Arabidops
37	718	63.5	166	3	AAG30423	AAG30423 Arabidops
38	714	63.1	257	8	ADY06189	ADY06189 Plant full
39	712	63.0	247	8	ADY22656	ADY22656 Plant full
40	712	63.0	247	8	ADY22656	ADY22656 Plant full
41	711	62.9	155	3	AAG37515	AAG37515 Arabidops
42	699	61.5	150	3	AAB32605	AAB32605 Eucalyptu
43	695	61.5	150	3	AAB32605	AAB32605 Eucalyptu
44	650	57.5	141	3	AAG37012	AAG37012 Arabidops
45	650	57.5	141	3	AAG37012	AAG37012 Arabidops
46	650	57.5	141	3	AAG37012	AAG37012 Arabidops
47	646.5	57.2	142	3	AAG31749	AAG31749 Arabidops
48	646	57.1	142	3	AAG31749	AAG31749 Arabidops
49	641	56.7	142	3	AAG40309	AAG40309 Arabidops
50	640	56.6	143	3	AAG44462	AAG44462 Arabidops
51	640	56.6	143	3	AAG44462	AAG44462 Arabidops
52	606	53.6	133	3	AAG47168	AAG47168 Arabidops
53	603	53.3	184	8	ADY15872	ADY15872 Plant full
54	557	49.2	207	8	ADY11571	ADY11571 Plant full
55	488	44.2	102	3	AAG37517	AAG37517 Arabidops
56	477	42.2	134	8	ADY6517	ADY6517 Arabidops
57	426	37.7	137	8	ADY6517	ADY6517 Arabidops
58	426	37.7	137	8	ADY6517	ADY6517 Arabidops
59	413.5	36.6	219	3	AAG05537	AAG05537 Arabidops
60	411.5	36.4	159	3	AAG30701	AAG30701 Arabidops
61	407	36.0	221	3	AAG17322	AAG17322 Arabidops
62	392	34.7	240	8	ADY04466	ADY04466 Plant full
63	392	34.7	240	8	ADY04466	ADY04466 Plant full
64	392	34.7	245	8	ADY10819	ADY10819 Plant full
65	389	34.4	245	8	ADY89634	ADY89634 Plant full
66	386	34.1	131	3	AAB32624	AAB32624 Eucalyptu
67	381	33.7	96	3	AAB32962	AAB32962 Pinus rad
68	380	33.6	220	4	AAG79106	AAG79106 Tetanus n
69	380	33.6	220	5	AAB84307	AAB84307 Human end
70	380	33.6	220	7	ADY59037	ADY59037 Human pro
71	380	33.6	220	7	ADY59034	ADY59034 Human pro
72	380	33.6	220	7	ADY59034	ADY59034 Human pro
73	380	33.6	220	7	ADY59034	ADY59034 Human pro
74	377.5	33.4	219	3	AAG30570	AAG30570 Arabidops
75	375.5	33.2	235	8	ADY04998	ADY04998 Plant full
76	375.5	33.2	276	8	ADY07331	ADY07331 Plant full
77	363	32.1	85	3	AAB32906	AAB32906 Pinus rad
78	349	30.9	406	8	ADY2707	ADY2707 Plant full
79	347.5	30.7	144	3	AAG30702	AAG30702 Arabidops
80	345	30.5	74	3	AAG47157	AAG47157 Arabidops
81	343.5	30.4	218	4	AAB58279	AAB58279 Arabidops
82	340	30.1	178	4	AAG20288	AAG20288 Arabidops
83	336	29.7	188	4	AAG79107	AAG79107 Amino aci
84	334	29.5	113	3	AAB32553	AAB32553 Eucalyptu
85	328.5	29.0	134	3	AAB31660	AAB31660 Arabidops
86	325	28.7	177	3	AAG17323	AAG17323 Arabidops
87	324	28.6	75	3	AAB32776	AAB32776 Eucalyptu
88	304	26.9	68	3	AAB32968	AAB32968 Pinus rad
89	303	26.8	77	3	AAB32944	AAB32944 Pinus rad
90	298.5	26.5	155	3	AAG17324	AAG17324 Arabidops
91	298.5	26.4	79	3	AAG20287	AAG20287 Arabidops
92	298.5	26.4	79	3	AAG47156	AAG47156 Arabidops
93	295	26.4	87	3	AAG20286	AAG20286 Arabidops
94	295	26.1	69	3	AAG40307	AAG40307 Arabidops
95	295	26.1	70	3	AAG27458	AAG27458 Arabidops
96	294	26.0	154	3	AAG05538	AAG05538 Arabidops
97	290	25.6	66	3	AAG47196	AAG47196 Arabidops

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OM protein - protein search, using sw model

Run on: March 2, 2006, 05:11:44 ; Search time 38 Seconds
(without alignments) 557.044 Million cell updates/sec

Title: US-10-767-701-44293

Perfect score: 1131

Sequence: 1 MGQSLIYAFVARGVTILAR.....IITALILILISVCHGRKCH 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1016	89.8	220 2 T00801	probable synaptob
2	995	88.0	221 2 F84741	probable synaptob
3	988.5	87.4	229 2 F86180	hypothetical prote
4	732.5	64.8	240 2 T47589	synaptobrevin-like
5	718	63.5	175 2 D86180	hypothetical prote
6	646.5	57.2	212 2 T04630	probable synaptob
7	413.5	36.6	219 2 B71423	synaptobrevin homo
8	411.5	36.4	159 2 C84647	hypothetical prote
9	377.5	33.4	219 2 JC7258	probable synaptob
10	377	33.3	69 2 E86180	vesicle-associated
11	295	26.1	60 2 D44088	hypothetical prote
12	274	24.2	60 2 T39073	hypothetical prote
13	200.5	17.7	121 2 S31250	synaptobrevin homo
14	185	16.4	117 2 S47654	synaptobrevin homo
15	185	16.4	223 2 S62059	synaptobrevin homo
16	175	15.5	109 2 T33239	synaptobrevin homo
17	174.5	15.4	115 2 E88504	synaptobrevin iso
18	174.5	15.4	719 2 UC1522	synaptobrevin iso
19	169.5	15.0	132 2 B38315	synaptobrevin 2 -
20	169.5	15.0	152 2 T33477	synaptobrevin 2 -
21	167.5	14.8	116 2 B34288	synaptobrevin 2 -
22	167.5	14.8	116 2 T33477	synaptobrevin 2 -
23	167.5	14.8	116 2 T33477	synaptobrevin 2 -
24	160	14.1	211 2 S52747	synaptobrevin 2 -
25	153	13.5	125 2 A58315	synaptobrevin 2 -
26	149.5	13.2	118 2 A58315	synaptobrevin 1 -
27	149.5	13.2	118 2 A58315	synaptobrevin 1 -
28	147	13.0	118 2 A58315	synaptobrevin 1 -
29	145.5	12.9	120 2 A52146	vehicle-associated

30	145.5	12.9	209 2 T40099	probable synaptob
31	145.5	12.9	251 2 S64937	probable membrane
32	143.5	12.7	103 2 S35077	cellulobrevin - rat
33	142	12.6	260 2 T09027	hypothetical prote
34	138.5	12.2	508 2 F86458	unknown protein, 7
35	136.5	12.1	198 2 TR0228	unknown protein, 7
36	128	11.3	254 2 T04067	hypothetical prote
37	128	11.3	253 2 C86253	hypothetical prote
38	120	10.6	145 2 T21318	hypothetical prote
39	118.5	10.5	197 2 T39412	hypothetical prote
40	115.5	10.2	110 2 S35107	hypothetical prote
41	114	10.1	200 2 T52162	hypothetical prote
42	111	9.8	200 2 S38053	probable snare pro
43	97	8.6	257 2 A89456	protein F55A4.1 [i
44	95	8.4	102 2 S44781	hypothetical prote
45	94.5	8.4	102 2 T24909	hypothetical prote
46	91	8.0	317 2 JC2110	hypothetical prote
47	89	8.0	559 2 A39793	hypothetical prote
48	89	8.0	2364 1 A44159	tropomyosin-relate
49	89	7.9	598 2 S28712	t-complex-type mol
50	89	7.9	336 2 D70360	spectrin beta-g ch
51	89	7.9	647 2 H89988	conserved hypochet
52	89	7.9	946 2 T08913	hypothetical prote
53	88	7.8	246 2 E70001	cell division prot
54	87	7.7	239 2 T16252	hypothetical prote
55	87	7.7	554 2 T46977	hypothetical prote
56	87	7.7	738 2 A40096	cell division cont
57	87	7.7	796 2 B84800	platelet-endothel
58	87	7.7	2166 2 G70163	probable alpha-car
59	86.5	7.6	461 2 D64701	hypothetical prote
60	86	7.6	196 2 A36554	thiophene and fura
61	85.5	7.6	214 2 T47779	ribosomal protein
62	85.5	7.6	463 2 T47779	synaptobrevin SEC2
63	85.5	7.6	812 2 A81621	hypothetical prote
64	85.5	7.6	831 2 F72044	conserved hypochet
65	85.5	7.6	831 2 C86581	C620 hypochetical
66	85	7.5	287 2 T25849	hypochetical prote
67	85	7.5	461 2 G71818	probable thiophene
68	84.5	7.5	1671 2 S71628	sensory transduct
69	84	7.4	284 2 T41624	probable syntaxin
70	84	7.4	290 2 C48213	syntaxin 2 - rat
71	84	7.4	930 2 A97932	initiation factor
72	84	7.4	958 2 G95064	translation initia
73	83.5	7.4	132 2 B31492	DNA-binding prote
74	83.5	7.4	205 2 A64373	hypochetical prote
75	83.5	7.4	246 1 S01789	formate acetyltran
76	83.5	7.4	246 2 G85615	pyruvate formate 1
77	83.5	7.4	246 2 A99752	hypochetical prote
78	83.5	7.4	292 2 T32000	ribosomal protein
79	83	7.3	196 1 RSRT19	ribosomal protein
80	83	7.3	196 1 A48992	hypochetical prote
81	83	7.3	816 2 S64439	ABC transporter, A
82	82.5	7.3	218 2 C97236	similar to chlorom
83	82.5	7.3	358 2 C96923	heat shock protein
84	82.5	7.3	598 2 S34203	DNA binding protei
85	82.5	7.3	678 2 S54308	3-oxoacyl-(acyl)-ca
86	82.5	7.3	764 2 H83879	cut14 protein - fi
87	82.5	7.3	1172 2 S51623	vacuolar protein V
88	82	7.3	283 2 S61664	hypochetical prote
89	82	7.3	1418 2 S64918	beta spectrin, bet
90	82	7.3	2388 2 JE0271	glucanin - human
91	82	7.3	3225 2 I52300	glucanin - human
92	82	7.3	3259 1 A56539	hypochetical prote
93	82	7.3	308 2 H81345	mitotic spindle as
94	81.5	7.2	1120 2 UC7765	myosin V - fruit f
95	81.5	7.2	1792 2 T13939	4-aminobutyrate am
96	81	7.2	216 1 K1BYT8	conserved hypochet
97	81	7.2	454 2 E75116	type I restriction
98	81	7.2	470 2 H82054	type I restriction
99	81	7.2	558 2 A64515	type I restriction
100	81	7.2	666 2 A72428	type I restriction
101	81	7.2	891 2 A38903	type I restriction
102	81	7.2	1104 2 B75221	type I restriction

RESULT 2
US-10-219-999-41251
Sequence 41251, Application US/10219999
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgeton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingsong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 41251
LENGTH: 220
TYPE: PRT
ORGANISM: Zea mays
US-10-219-999-41251

Query Match 100.0%; Score 1131; DB 32; Length 220;
Best Local Similarity 100.0%; Pred. No. 3.9e-100;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGQSLIYAFVARGVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDDHTFNLYVE 60
DB 1 MGQSLIYAFVARGVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDDHTFNLYVE 60
QY 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKYGGRATTAANSLNREFSGKLKEHMOY 120
DB 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKYGGRATTAANSLNREFSGKLKEHMOY 120
QY 121 CVDHPEEYSKLAKVAQVSEVGVMMENIEKVLDRGEKIELVDKTEMLRSQADPROG 180
DB 121 CVDHPEEYSKLAKVAQVSEVGVMMENIEKVLDRGEKIELVDKTEMLRSQADPROG 180
QY 181 TNVRRKMWLQNNKIKLIVLGIIIALIIILISVCHGFKCH 220
DB 181 TNVRRKMWLQNNKIKLIVLGIIIALIIILISVCHGFKCH 220

RESULT 3
US-10-219-999-54339
Sequence 54339, Application US/10219999
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgeton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingsong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 54339
LENGTH: 220
TYPE: PRT
ORGANISM: Zea mays
US-10-219-999-54339

Query Match 100.0%; Score 1131; DB 32; Length 220;
Best Local Similarity 100.0%; Pred. No. 3.9e-100;

Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGQSLIYAFVARGVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDDHTFNLYVE 60
DB 1 MGQSLIYAFVARGVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDDHTFNLYVE 60
QY 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKYGGRATTAANSLNREFSGKLKEHMOY 120
DB 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKYGGRATTAANSLNREFSGKLKEHMOY 120
QY 121 CVDHPEEYSKLAKVAQVSEVGVMMENIEKVLDRGEKIELVDKTEMLRSQADPROG 180
DB 121 CVDHPEEYSKLAKVAQVSEVGVMMENIEKVLDRGEKIELVDKTEMLRSQADPROG 180
QY 181 TNVRRKMWLQNNKIKLIVLGIIIALIIILISVCHGFKCH 220
DB 181 TNVRRKMWLQNNKIKLIVLGIIIALIIILISVCHGFKCH 220

RESULT 4
US-10-425-115-193538
Sequence 193538, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 193538
LENGTH: 220
TYPE: PRT
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: MFT4577_108090C.1.pcp
US-10-425-115-193538

Query Match 100.0%; Score 1131; DB 34; Length 220;
Best Local Similarity 100.0%; Pred. No. 3.9e-100;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGQSLIYAFVARGVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDDHTFNLYVE 60
DB 1 MGQSLIYAFVARGVILAEYTEFTGNFTTASQCLMKLPASNNKFTYNCDDHTFNLYVE 60
QY 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKYGGRATTAANSLNREFSGKLKEHMOY 120
DB 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKYGGRATTAANSLNREFSGKLKEHMOY 120
QY 121 CVDHPEEYSKLAKVAQVSEVGVMMENIEKVLDRGEKIELVDKTEMLRSQADPROG 180
DB 121 CVDHPEEYSKLAKVAQVSEVGVMMENIEKVLDRGEKIELVDKTEMLRSQADPROG 180
QY 181 TNVRRKMWLQNNKIKLIVLGIIIALIIILISVCHGFKCH 220
DB 181 TNVRRKMWLQNNKIKLIVLGIIIALIIILISVCHGFKCH 220

RESULT 5
US-10-767-701-44293
Sequence 44293, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701